









APPLICANT: MOIR, Christine  
 APPLICANT: Woodland, Christine  
 APPLICANT: Reichenbach, Christine  
 APPLICANT: Reichenbach, Christine  
 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSWAMI  
 NUMBER OF SEQUENCES: 1152  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: MO, 2144444 Corporation  
 CITY: Research Triangle Park  
 STATE: NC 27709  
 COUNTRY: USA  
 COMPUTER READABLE FORM:  
 COPIES: 1  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Release #1.0, Version #1.30  
 APPLICATION NUMBER: US/08/998,416  
 FILING DATE: 24-DEC-1997  
 PRIORITY DATE: 24-DEC-1997  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: CH 0016/97  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WEISS, J. Timothy  
 TELEPHONE: 919-541-8897  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-541-8897  
 INFORMATION FOR SEQ ID NO: 535:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: nucleic acid  
 STRANDNESS: single  
 TOPOLOGY: linear  
 ORGANISM: Aspergillus fumigatus  
 ORIGINAL SOURCE: DNA (genomic)  
 ORGANISM: ENGL13HP  
 US-08-998-416-535  
 Query Match 2.1% Score 43.4; DB 1; Length 827;  
 Best Local Similarity 43.0%; Pval: No. 0.025;  
 Matches 200; Conservative 0; Mismatches 265; Indels 0; Gaps 0;  
 Oy 1098 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1157  
 Db 216 atgaaacattttatgacgctttatgaaacacgaagcttgatgaagcttacc 1157  
 Oy 1158 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1217  
 Db 276 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1217  
 Oy 1218 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1277  
 Db 336 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1395  
 Oy 1278 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1337  
 Db 386 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1397  
 Oy 1318 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1397  
 Db 456 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1457  
 Oy 1358 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1457  
 Db 516 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1515

Oy 1458 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1517  
 Db 576 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1517  
 Oy 1518 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1562  
 Db 636 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1680  
 RESULT 8  
 US-07-885-9704-247  
 TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON  
 GENERAL INFORMATION:  
 INVENTOR: KIM, J. Y. W. E.  
 NUMBER OF SEQUENCES: 33  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: KIM, J. Y. W. E.  
 STREET: P. O. Box 2113, First Wisconsin Plaza  
 CITY: Madison  
 STATE: WI 53706  
 COUNTRY: USA  
 COMPUTER READABLE FORM:  
 COPIES: 1  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Microsoft Word  
 APPLICATION NUMBER: US/07/885,970A  
 FILING DATE: 21-NOV-1990  
 PRIORITY DATE: 21-NOV-1990  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/417,239  
 FILING DATE: 04-OCT-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SEAY, Nicholas J.  
 TELEPHONE: (608) 281-2478  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (608) 281-2478  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: nucleic acid  
 STRANDNESS: double  
 TOPOLOGY: linear  
 ORGANISM: Gossypium hirsutum  
 ORIGINAL SOURCE: Cella protoplasts  
 ORGANISM: Cella protoplasts  
 COUNTRY: CP  
 US-07-885-9704-24  
 Query Match 2.1% Score 43; DB 1; Length 1618;  
 Best Local Similarity 55.8%; Pval: No. 0.045; 55; Indels 0; Gaps 0;  
 Matches 82; Conservative 0; Mismatches 155;  
 Oy 1160 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1235  
 Db 149 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1235  
 Oy 1458 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1299  
 Db 89 atgtatgacgctctttatgagtcgaacacgaagcttgatgaagcttacc 1300













GeoCore version 4.5  
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OK nucleic - nucleic search, using sw model

Run on: August 18, 2001, 22:01:01 : Search time 5406.15 seconds

5784,396 Million cell updates/sec

File: us-09-284-320-56

Perfect score: 2033

Sequence: 1 gagctcgagcgctccctc.....gttaatgatgacaaac 2033

Scoring Table: IDENTITY, MJC

Gapop 10.0, Gapext 1.0

Searched: 134457 seqs, 77387458 residues

Total number of hits satisfying chosen parameters: 268314

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank1:

1: gb-ba1.\*  
2: gb-ba2.\*  
3: gb-ba3.\*  
4: gb-ba4.\*  
5: gb-ba5.\*  
6: gb-ba6.\*  
7: gb-ba7.\*  
8: gb-ba8.\*  
9: gb-ba9.\*  
10: gb-ba10.\*  
11: gb-ba11.\*  
12: gb-ba12.\*  
13: gb-ba13.\*  
14: gb-ba14.\*  
15: gb-ba15.\*  
16: gb-ba16.\*  
17: gb-ba17.\*  
18: gb-ba18.\*  
19: gb-ba19.\*  
20: gb-ba20.\*  
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36: gb-ba36.\*  
37: gb-ba37.\*  
38: gb-ba38.\*  
39: gb-ba39.\*  
40: gb-ba40.\*  
41: gb-ba41.\*  
42: gb-ba42.\*  
43: gb-ba43.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and is derived by analysis of the total score distribution.

# SUMMARIES

No.	Score	Match	Length	DB ID	Description
1	1023	92.2	1884	93	AF248565 Homo sapi
2	1474.8	92.2	1884	93	AF248565 Homo sapi
3	1429.8	70.3	158239	80	AL353115 Homo sapi
4	1428.2	70.3	158517	80	AL353115 Homo sapi
5	1428.2	70.3	158517	80	AL353115 Homo sapi
6	1078	53.0	126543	66	AC026156 Homo sapi
7	622	36.6	422	97	U17925 Homo sapi
8	376.5	16.6	513	54	U17925 Homo sapi

[illegible]













```

Db 198213 -TATGATGCTTTATATATACACCAAAATC-----ATATGAGCATATACAC 198167
Oy 1865 TAAAGATTTATTCGAGAAATTCCTCCCGTGAGTACAGATGATTTGATGAGCA 1924
Db 198166 TAAAGATTTATTCGAGAAATTCCTCCCGTGAGTACAGATGATTTGATGAGCA 198107
Oy 1925 TATTCATGATGAGAAATTCCTCCCGTGAGTACAGATGATTTGATGAGCA 1984
Db 198106 TATTCATGATGAGAAATTCCTCCCGTGAGTACAGATGATTTGATGAGCA 198052
Oy 1985 AACCATATGAGTACAGATGATTTGATGAGCA 203
Db 198051 ACTGTCATGAGTACAGATGATTTGATGAGCA 198023
RESULT 5
LOCUS 3818/c
DEFINITION Homo sapiens chromosome 1 clone RP11-294M, *** SEQUENCING IN
ACCESSION U00009894
VERSION 1
KEYWORDS HTS; HTS; HARET; HTS; DMAT.
ORGANISM Homo sapiens
Bukhari:Choudhri;Gentile;Verobral;EutelsioLocal:
Mammalia;Eutheria;Primates;Carnivora;Homidae;Homo.
Strain:RP11-294M
Plasmid-B.
Direct Submission
Accession:U00009894
Requester:clonerequest@anger.ac.uk
On Sep 9, 2000 this sequence version replaced g1:9797313.
COMMENT
Center: Sanger Centre
Contact: hamper@anger.ac.uk
Project information
Assembly program: NCBI, version 4.5
Consensus quality: 151504 bases at least Q40
Consensus quality: 151504 bases at least Q40
Insert size (kb): 16280 bases at least Q40
Insert size (kb): 17457; 3.8 error; average-fp
Insert coverage: 4.23x in Q40 bases; sum-of-coverage quality
Insert coverage: 4.23x in Q40 bases; average-fp
NOTE: This is a working draft sequence. It currently
is not known and their order in this sequence record as
arbitrary. Gaps between the contigs are represented as
XXXXXXXXXX. The length of the contigs is unknown.
This record will be updated as the reference sequence
as soon as it is available and the accession number will
be preserved.
8110: contig of 8110 bp in length
8211: contig of 100 bp
8211: 1884: contig of 564 bp in length
1395: 4693: contig of 3193 bp in length
4693: 47093: gap of 100 bp
5704: 5955: contig of 12421 bp in length
5704: 5955: contig of 2703 bp in length
8681: 8691: gap of 100 bp
8681: 8691: gap of 100 bp
9006: 9015: contig of 100 bp
9006: 9015: gap of 100 bp

```

## FEATURES

```

source
10165..10186: contig of 1163 bp in length
10189..10198: gap of 100 bp
10199..10570: contig of 3512 bp in length
10571..10591: gap of 100 bp
10592..10921: contig of 100 bp in length
10922..11386: contig of 4378 bp in length
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GENOTYPE: HMO, RTGS, PKRSET, RTGS, DNAT.

ORGANISM: Homo sapiens

REFERENCE: 1 (bases 1 to 126533) GenBank: U00001.1

ATTNOS: Lu, G., Zhou, Y., Lin, W., Dong, H., Zhou, M., Xu, S., Gu, W., Tu, Y., Wang, X., Zhang, C., Zhou, M., Zhou, Y., Wei, S., Fu, G., Chen, Z., and Huang, K.

TITLE: Direct Submission

JOURNAL: Submitted (21-MAR-2000) Genomic Dept., Chinese National Human Genome Center at Shanghai, 201203, P. R. China

COMMENT: On Mar 26, 2000 this sequence version replaced g1:721971.

Center: Chinese National Human Genome Center at Shanghai

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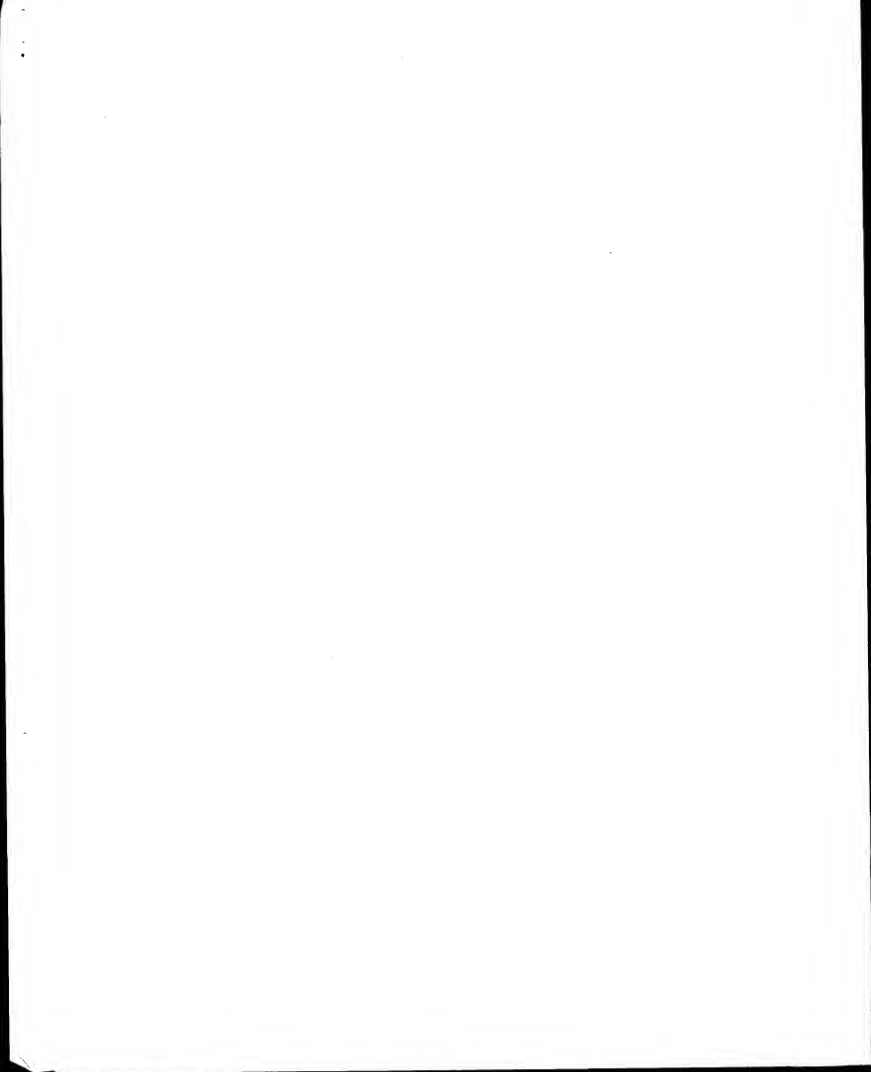






















CORRESPONDENCE ADDRESS:  
 COMPANY: Pharmacia, Inc.  
 STREET: 4000 Bell Atlantic Tower, 1117 Arch Street  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103-2793  
 COMPUTER READABLE FORM:  
 OPERATING SYSTEM: DOS  
 COMPUTER: IBM Compatible  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/961,519  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dickinson, O. Todd  
 REGISTRATION NUMBER: 28,354  
 REFERENCE/DOCKET NUMBER: GM1014  
 TELEPHONE: 215/994-2252  
 TELEFAX: 215/994-2420  
 TELEX:  
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 APPLICANT: Brown, James R.  
 TITLE OF INVENTION: No. 6171840a1 Inac  
 NUMBER OF SEQUENCES: 7  
 OPERATING SYSTEM: DOS  
 ADDRESSER: Dechert, Prince & Rhoads  
 STREET: 4000 Bell Atlantic Tower, 1117 Arch Site  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103-2793  
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 OPERATING SYSTEM: DOS  
 COMPUTER: IBM Compatible  
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 ATTORNEY/AGENT INFORMATION:  
 NAME: Dickinson, O. Todd  
 REGISTRATION NUMBER: 28,354  
 REFERENCE/DOCKET NUMBER: PF-0002 US  
 TELEPHONE: 215/994-2252

SOFTWARE: FASTED for Windows version 2.0  
 COMPANY: Pharmacia, Inc.  
 STREET: 4000 Bell Atlantic Tower, 1117 Arch Street  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103-2793  
 COMPUTER READABLE FORM:  
 OPERATING SYSTEM: DOS  
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 ATTORNEY/AGENT INFORMATION:  
 NAME: Dickinson, O. Todd  
 REGISTRATION NUMBER: 28,354  
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RESULT 9  
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 APPLICANT: Aeridium, Ingrid E.  
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 ADDRESSER: Pharmacia, Inc.  
 STREET: 1174 Porter Drive  
 STATE: CA  
 COUNTRY: U.S.  
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 ATTORNEY/AGENT INFORMATION:  
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 REGISTRATION NUMBER: 28,354  
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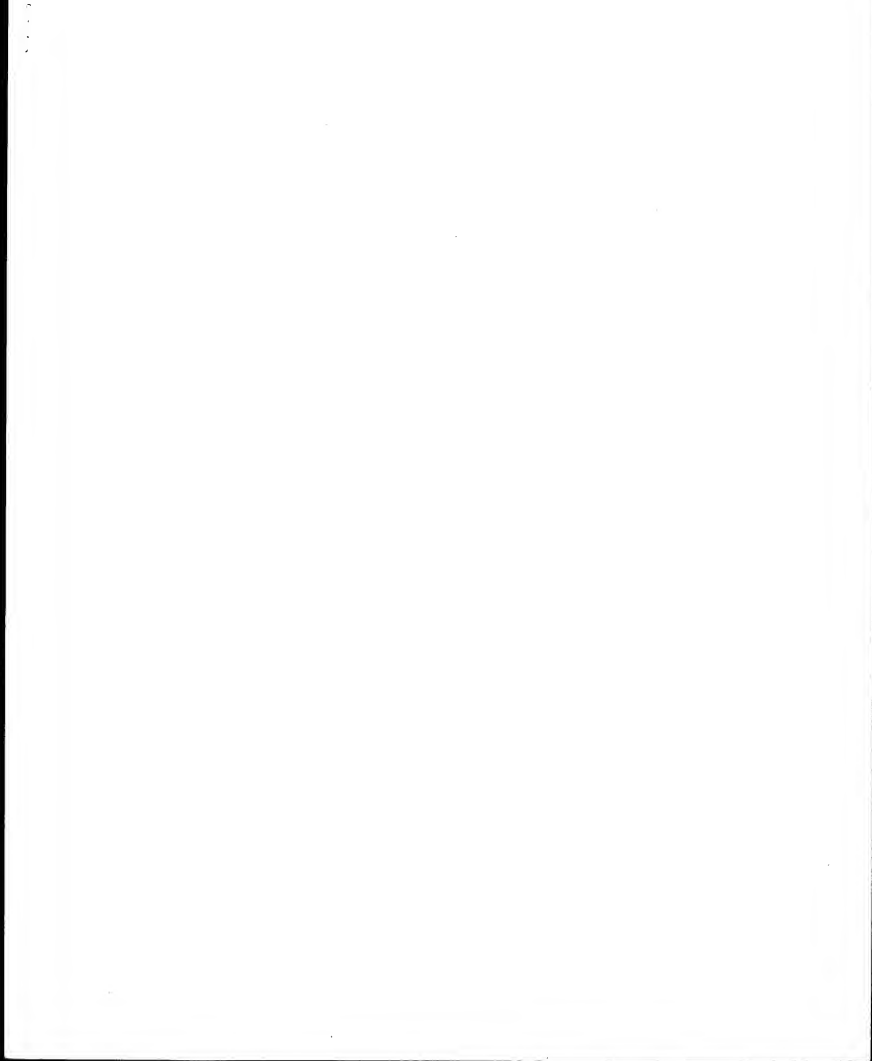




1 TITLE OF INVENTION: 11-3  
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 3 CORRESPONDENCE ADDRESS:  
 4 STREET: 725 UNIVERSITY AVENUE  
 5 CITY: Palo Alto  
 6 STATE: California  
 7 ZIP: 94304-1018  
 8 COMPUTER READABLE FORM: 4188  
 9 COMPUTER: IBM PC compatible  
 10 OPERATING SYSTEM: PC-DOS/MS-DOS  
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 48 GENERAL INFORMATION:  
 49 APPLICANT: Marcus D. Ballinger and James A. Wells  
 50 TITLE OF INVENTION: SUBSTRATES CONTAINING DIANIC RESIDUES  
 51 NUMBER OF SEQUENCES: 74  
 52 CORRESPONDENCE ADDRESS:  
 53 STREET: 1 DOW WAY  
 54 CITY: South San Francisco  
 55 STATE: California  
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252:  qb-as173.*
253:  qb-as174.*
254:  qb-as175.*
255:  qb-as176.*
256:  qb-as177.*
257:  qb-as178.*
258:  qb-as179.*

```

Print. No. is the number of results predicted by chance to have a  
 given score. The number of results predicted by chance to have a  
 given score is printed to the right of the result being printed,  
 and is derived by analysis of the total score distribution.



























Mon Aug 20 10:21:38 2001

us-09-284-320-31.rst

Page 14















```

OT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment ERD NO: 10141.
DE Protein identification: signal transduction pathway;
KW hydrolase; protein; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX ERD3405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000: 2000EP-0104139.
XX
XX 25-FEB-1999: 9905-0121835.
XX 09-MAY-1999: 9905-0122580.
XX 23-MAY-1999: 9905-0125788.
XX 29-MAY-1999: 9905-0126244.
XX 01-APR-1999: 9905-0127462.
XX 06-SEP-1999: 9905-0128214.
XX 16-SEP-1999: 9905-0128655.
XX 19-FEB-1999: 9905-0130077.
XX 23-FEB-1999: 9905-0130510.
XX 28-FEB-1999: 9905-0130891.
XX 30-FEB-1999: 9905-0132407.
XX 04-MAY-1999: 9905-0132484.
XX 06-MAY-1999: 9905-0132486.
XX 11-MAY-1999: 9905-0132633.
XX 14-MAY-1999: 9905-0132718.
XX 14-MAY-1999: 9905-0132719.
XX 18-MAY-1999: 9905-0132768.
XX 20-MAY-1999: 9905-0133121.
XX 21-MAY-1999: 9905-0133531.
XX 24-MAY-1999: 9905-0135629.
XX 25-MAY-1999: 9905-0135700.
XX 27-MAY-1999: 9905-0135702.
XX 28-MAY-1999: 9905-0136782.
XX 01-JUN-1999: 9905-0137524.
XX 04-JUN-1999: 9905-0137502.
XX 10-JUN-1999: 9905-0138540.
XX 10-JUN-1999: 9905-0138617.
XX 16-JUN-1999: 9905-0139462.
XX 16-JUN-1999: 9905-0139462.
XX 18-JUN-1999: 9905-0139465.
XX 18-JUN-1999: 9905-0139466.
XX 18-JUN-1999: 9905-0139467.
XX 18-JUN-1999: 9905-0139468.
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XX 18-JUN-1999: 9905-0139470.
XX
XX 18-JUN-1999: 9905-0139763.
XX 21-JUN-1999: 9905-0139817.
XX 22-JUN-1999: 9905-0139899.
XX 23-JUN-1999: 9905-0140353.
XX 24-JUN-1999: 9905-0140655.
XX 26-JUN-1999: 9905-0140823.
XX 30-JUN-1999: 9905-0141287.
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XX 06-JUL-1999: 9905-0142603.
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XX 20-AUG-1999: 9905-0149493.
XX 23-AUG-1999: 9905-0149802.
XX 25-AUG-1999: 9905-0150565.
XX 26-AUG-1999: 9905-0150884.

```









Disclature: Page 56-61, 87pp; English.

CC Human neurofibromatosis type 1 (NF1)-GAP related domain (GRD) was  
CC cloned into the yeast expression vector pX10 to obtain pX11. The  
CC pX11 DNA was mutagenized by hydroxylation in vitro and transformed  
CC into *S. cerevisiae* TK101-R27-D, which carries an oncogenic-type  
CC RSV-D, and screened for the heat shock sensitivity of the clones was  
CC checked. Plasmid DNAs were recovered, re-transformed into TK101-  
CC R27-D, and phenotypic reversion was examined. 2 Clones, NF201 and  
CC NF202, given in A85921, which had strong suppression activity for  
CC NF1, were selected. The mutant NF1-GDs were also able to  
CC inhibit v-Has-induced transformation in mammalian cells.

Sequence 2485 AA:

Query Match 5.7% Score 100.5; Db 15; Length 2485;

Best Local Similarity 22.24; Pred. No. 3.9; Indeks 101; Gaps 18;

Matches 86; Conservative 60; Mismatches 140; Indels 101; Gaps 18;

13 GINVERPILASPSVYRNRMNPFPE-----RIPDAKSMGFVWDLSMGLAY 65

1667 gqqlqkewadavalsapnvlvskaygimckldkclspklqghlmdadl 1726

66 GINFRPAAVWVWGVGNLALPFG-----SVISPLKAWVPSLDS-----VANSINS 115

1277 -----larpmlstfnadvaahlylthvvt-lvaqqlstaahtqlyvalhla 1778

116 L-----FSEKPPVQLAASG--SEVWQKANSFPEDSVTLR-QLNRSLPDSNY 164

1779 lctcqhlfseetkqylrlstetlptkylqlqskasavlatfsydydftspy 1838

165 -LSRPSLSRNRPDLASLQVLDLIDSL--LSRHMLAK-----DISPDLSLELA 217

1839 eretclstetva-lleam-acmdptkcdvvelatqatfayspatly 1896

218 GIDRTGRK-VGRSDRFRKALSLVDLQKGFQWMS----- 253

1897 vqicqlhfsesqylrlstetlptkylqlqskasavlatfsydydftspy 1954

254 -----LGNQNVPL--VWNSQGTSLAKRTTLKAAQANPSF----- 292

1955 apklalvtvavqlgdevnlpasqqlhldhlllslatrlndpsvfnaltrpale 2014

293 -----VNAKXKRETSVPSNW 310

2015 whkqghltvqldfrnltatqyll 2041

RESULT 14

ID A85922 standard: protein: 2485 AA.

AM85922:

22-FEB-1995 (first entry)

HAS associated GM. N204.

Has: GTPase activating protein; GAP; GAP related domain; GRD;

DEFECT (NF1), Schwannoma; cerebellar; RAS2; v-Has; heat shock;

DEFECT (NF2), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF3), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF4), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF5), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF6), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF7), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF8), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF9), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF10), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF11), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF12), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

(SCHE ) SCHERING CORP.

Kazuo Y, Nakafuku M.

WPI: 1994-249216/70.

Blocking Ras-induced effects on a cell - by introducing a GTPase

activating protein to the cell, using Gap. In treatment of cancer

Disclature: Page 44-52, 87pp; English.

CC Human neurofibromatosis type 1 (NF1)-GAP related domain (GRD) was  
CC cloned into the yeast expression vector pX10 to obtain pX11. The  
CC pX11 DNA was mutagenized by hydroxylation in vitro and transformed  
CC into *S. cerevisiae* TK101-R27-D, which carries an oncogenic-type  
CC RSV-D, and screened for the heat shock sensitivity of the clones was  
CC checked. Plasmid DNAs were recovered, re-transformed into TK101-  
CC R27-D, and phenotypic reversion was examined. 2 Clones, NF201 and  
CC NF202, given in A85921, which had strong suppression activity  
CC to inhibit v-Has-induced transformation in mammalian cells.

Sequence 2485 AA:

Query Match 5.7% Score 100.5; Db 15; Length 2485;

Best Local Similarity 22.24; Pred. No. 3.9; Indeks 101; Gaps 18;

Matches 86; Conservative 60; Mismatches 140; Indels 101; Gaps 18;

13 GINVERPILASPSVYRNRMNPFPE-----RIPDAKSMGFVWDLSMGLAY 65

1667 gqqlqkewadavalsapnvlvskaygimckldkclspklqghlmdadl 1726

66 GINFRPAAVWVWGVGNLALPFG-----SVISPLKAWVPSLDS-----VANSINS 115

1277 -----larpmlstfnadvaahlylthvvt-lvaqqlstaahtqlyvalhla 1778

116 L-----FSEKPPVQLAASG--SEVWQKANSFPEDSVTLR-QLNRSLPDSNY 164

1779 lctcqhlfseetkqylrlstetlptkylqlqskasavlatfsydydftspy 1838

165 -LSRPSLSRNRPDLASLQVLDLIDSL--LSRHMLAK-----DISPDLSLELA 217

1839 eretclstetva-lleam-acmdptkcdvvelatqatfayspatly 1896

218 GIDRTGRK-VGRSDRFRKALSLVDLQKGFQWMS----- 253

1897 vqicqlhfsesqylrlstetlptkylqlqskasavlatfsydydftspy 1954

254 -----LGNQNVPL--VWNSQGTSLAKRTTLKAAQANPSF----- 292

1955 apklalvtvavqlgdevnlpasqqlhldhlllslatrlndpsvfnaltrpale 2014

293 -----VNAKXKRETSVPSNW 310

2015 whkqghltvqldfrnltatqyll 2041

RESULT 15

ID A852268 standard: Protein: 2818 AA.

A852268:

06-MAR-1992 (first entry)

NIH gene product.

von Recklinghausen neurofibromatosis disease; autosomal dominant;

gene therapy.

Defect (NF1), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF2), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF3), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF4), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

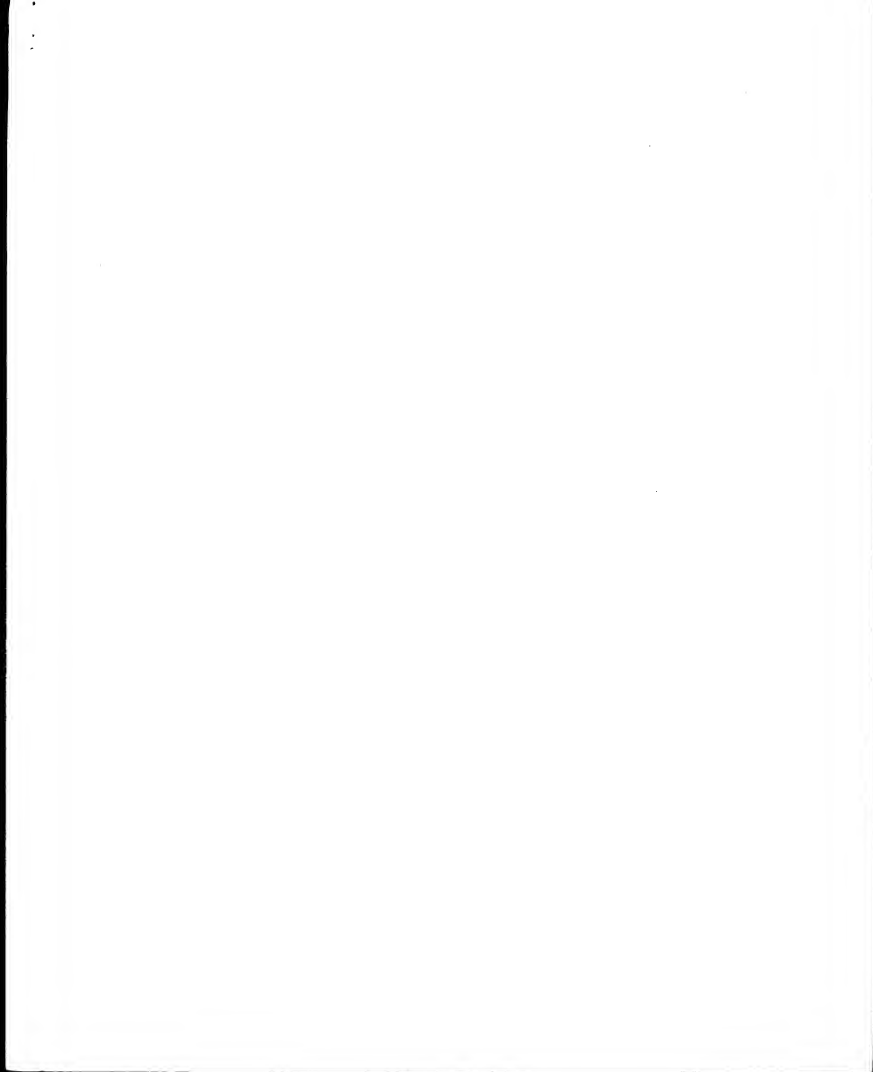
Defect (NF5), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;

Defect (NF6), v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has; v-Has;



PN M09200387.A.  
 PD 09-JUN-1992.  
 XX 28-JUN-1991: 91MO-0504634.  
 XX 29-JUN-1990: 90US-0547090.  
 PR (UMM ) UNIV OF MICHIGAN.  
 XX Collins ES, Wallace MR, Marcink DA, Andersen LB, Gutman DH;  
 PT WPI 1992-04566/05.  
 DR N-PSDB: A020602.  
 XX DNA sequences to vonRecklinghausen neurofibromatosis gene - and  
 PT derived amino acid sequences and probes for screening NFI in early  
 PT stages of disease  
 XX  
 PS Claim 25: Page 57; 12zpp: English.  
 XX This is the amino acid sequence of the von Recklinghausen neuro-  
 CC fibromatosis (NFI) gene product. It and antibodies raised against it  
 CC can be used in hybridisation and immunological assays to screen for  
 CC the presence of a normal or defective NFI gene product. Functional  
 CC assays have been developed to identify patients at risk for  
 CC diagnosis or to monitor treatment. Patient therapy through  
 CC supplementation with the normal NFI product which can be  
 CC produced by recombinant techniques is also possible.  
 XX  
 S0 Sequence 2818 AA:  
 Query Match 5.74; Score 100.5; DB 13; Length 2818;  
 Best Local Similarity 22.24; Pred. No. 4.8;  
 Matches 46; Conservative 60; Mismatches 140; Indels 101; Gaps 18;  
 Oy 13 CUGGCTSLKSPGVNPNMPICE-----KIPDVALSKGVSEGLSPGLAY 65  
 Db 2000 gqjgktaewakataalagayklyskaygcmkldcrlcpqlqplmaddai 2059  
 Oy 66 GUNFPEPATVWVYKGNVATLPPG---SYSPLENAVPSLDS---VANSHIS 115  
 Db 2060 -----lartphlslfnslavaahlylthvyl-lvarqplslrslshlyvnl 111  
 Oy 116 l-----PSTPTVGLAASE---EAYVGCANSPFEDLQVTR-QLAHN-PORNY 164  
 Db 2112 lccclqlhfeekpyrlsltelafpyllfglskvaaylafrasydrstsegyy 2171  
 Oy 165 -LSIPPLNLSKSNNDLPLRSLQVLDLDSL-LSRRLKAK-----DHSPTVSLDA 217  
 Db 2172 arellalalevlea-lleame-amcdpckldqvelqqlfaypalspraly 2229  
 Oy 218 GIDETCKK--YGGSDGPFQASRLVDAQKFDKWS-----SSTSS 253  
 Db 2230 vfgclskvsgqslqllslskaslecl--gqclgspylleavtalcklqplnd 2287  
 Oy 234 -----LVGNMVEL--VYVSPGTLIRKPTLLAKQANPSP----- 292  
 Db 2288 qphkalewawvayqewvlypsqslqlqhlslslrlfndpewvmafrpde 2347  
 Oy 293 -----VILAYVREVSVPWV 310  
 Db 2348 whckpdlfvgllfnmlfclayhll 2374

Search completed: July 3, 2001, 16:18:21  
 Job time: 168 sec









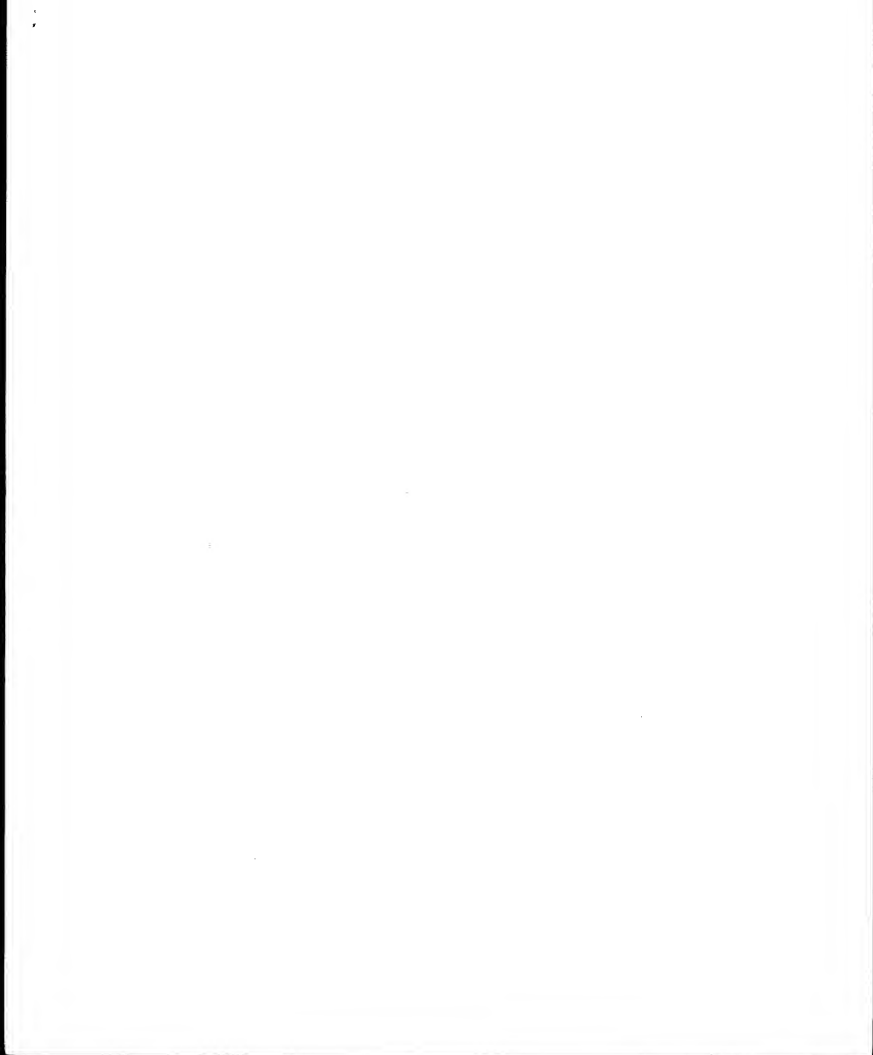












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Genome version 4.5

OM protein - protein search, using sw model

Run on: July 3, 2001, 16:17:23 / Search time 12.1 seconds

990,861 Million cell updates/sec

Title: US-09-284-320-6

Sequence: 1 MAFVYVLTAVYGVGMEFRS.....MDGVDSITVWTKIKMD 350

Scoring table: BLASTING2

Gap: 10.0, Gapext 0.5

Search: 9343 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100

Listing first 45 summaries

Database: Swissprot\_39+\*

Panel No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Summary:

No.	Score	Match	Length	ID	Description
1	513	29	1	VWLN_HUMAN	O75787 homo sapien
2	102	6	0	PROT_HUMAN	P13066 alpha
3	102	6	0	PROT_HUMAN	P13066 alpha
4	103	5	9	V150_HUMAN	P05618 helio
5	103	5	9	V150_HUMAN	P05618 helio
6	100	5	7	SH4_YEAST	P13178 sec
7	100	5	8	MYO1_MOUSE	P12449 mus
8	100	5	7	SH4_YEAST	P13178 sec
9	99	5	6	STY1_MOUSE	P12449 mus
10	98	5	6	STY1_MOUSE	P12449 mus
11	98	5	6	STY1_MOUSE	P12449 mus
12	97	5	5	MYO2_HUMAN	P12883 homo
13	97	5	5	MYO2_HUMAN	P12883 homo
14	97	5	5	MYO2_HUMAN	P12883 homo
15	96	5	5	MYO2_HUMAN	P12883 homo
16	96	5	5	MYO2_HUMAN	P12883 homo
17	96	5	5	MYO2_HUMAN	P12883 homo
18	95	5	4	MYO2_HUMAN	P12883 homo
19	95	5	4	MYO2_HUMAN	P12883 homo
20	94	5	4	MYO2_HUMAN	P12883 homo
21	93	5	3	MYO2_HUMAN	P12883 homo
22	93	5	3	MYO2_HUMAN	P12883 homo
23	93	5	3	MYO2_HUMAN	P12883 homo
24	91	5	2	MYO2_HUMAN	P12883 homo
25	91	5	2	MYO2_HUMAN	P12883 homo
26	91	5	2	MYO2_HUMAN	P12883 homo
27	91	5	2	MYO2_HUMAN	P12883 homo
28	90	5	1	MYO2_HUMAN	P12883 homo
29	90	5	1	MYO2_HUMAN	P12883 homo
30	90	5	1	MYO2_HUMAN	P12883 homo
31	90	5	1	MYO2_HUMAN	P12883 homo
32	90	5	1	MYO2_HUMAN	P12883 homo
33	90	5	1	MYO2_HUMAN	P12883 homo

34	90	5	1	MYO2_HUMAN	P12883 homo
35	90	5	1	MYO2_HUMAN	P12883 homo
36	89	5	1	MYO2_HUMAN	P12883 homo
37	89	5	1	MYO2_HUMAN	P12883 homo
38	89	5	1	MYO2_HUMAN	P12883 homo
39	89	5	1	MYO2_HUMAN	P12883 homo
40	89	5	1	MYO2_HUMAN	P12883 homo
41	89	5	1	MYO2_HUMAN	P12883 homo
42	89	5	1	MYO2_HUMAN	P12883 homo
43	88	5	0	MYO2_HUMAN	P12883 homo
44	88	5	0	MYO2_HUMAN	P12883 homo
45	87	5	0	MYO2_HUMAN	P12883 homo

ALIGNMENTS

RESULT 1

ID: VWLN\_HUMAN STANDARD: PR: 100 AA.

AC: O75787: 200 (rel. 39, Created)

DT: 30-MAY-2000 (rel. 39, Last annotation update)

DT: 01-OCT-2000 (rel. 40, Last annotation update)

DR: VANDOLAN\_AVE SYNTHESIS MEMBRANE SKELETON ASSOCIATED PROTEIN MR-9

OS: Homo sapiens (human).

OC: Bkaryota; Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi;

OX: NCBI\_Taxid=9606

BN: [1]

RF: Ludwig J. Schaefer H., Boyd A., Apps D.K.;

RL: Submitted (Aug-1998) to the EMBL/GenBank/ODD databases.

CC: -1- FUNCTION: VANDOLAN AVEPIS IS RESPONSIBLE FOR ADAPTATING A VARIETY

CC: -1- SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.

CC: -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC: THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION

CC: BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -

CC: THE EUROPEAN BIOINFORMATICS INSTITUTE. THESE TWO INSTITUTIONS DO NOT

CC: MODIFIED THIS STATEMENT IS NOT REMOVED. Usage by and for commercial

CC: ENTITIES require a license agreement (see <http://www.isb-ibc.com/license/>)

CC: -1- Entry date: 1998-08-11

DR: BMBJ: V17975; CMT6944.1;

FM: TRANSLATED BY: 79 TRANSLATED: TRANSAMBRIZNE.

DR: BMBJ: V17975; CMT6944.1;

SEQUENCE 100 AA: 11575 MW A070507B6576DC CRK64:

Query Match: 29.1%; Score 513; DB 1; Length 100;

Best Local Similarity: 100.0%; Prev. Num: 1; Len: 100;

Matches: 100; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

DB: 251 MAFVYVLTAVYGVGMEFRS...MDGVDSITVWTKIKMD 350

DB: 1 MAFVYVLTAVYGVGMEFRS...MDGVDSITVWTKIKMD 350

DB: 63 MAFVYVLTAVYGVGMEFRS...MDGVDSITVWTKIKMD 350

DB: 1 MAFVYVLTAVYGVGMEFRS...MDGVDSITVWTKIKMD 350

DB: 1 MAFVYVLTAVYGVGMEFRS...MDGVDSITVWTKIKMD 350

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DB: 1 MAFVYVLTAVYGVGMEFRS...MDGVDSITVWTKIKMD 350

18 VACUOLAR ATP SYNTHASE MEMBRANE SECTOR ASSOCIATED PROTEIN 98-5  
 19 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 20 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 21 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 22 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
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18 VACUOLAR ATP SYNTHASE MEMBRANE SECTOR ASSOCIATED PROTEIN 98-5  
 19 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
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 28 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
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 30 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 31 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 32 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 33 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 34 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 35 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 36 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 37 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 38 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 39 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 40 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 41 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 42 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 43 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 44 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 45 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 46 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
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 48 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 49 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)  
 50 (V-ATPASE 98-5) SUBUNIT 1 (EUROPEAN)























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OM protein - protein search, using SW model

Run on: July 3, 2001, 16:17:48 ; Search time 28.21 Seconds

1641502 Million cell updates/sec

Title: US-09-284-320-6

Sequence: 1 M95VWLLAVGCLGKLFERS.....M9GDSIIYRNTKIRMD 350

Scoring table:

Gap: 10.0, expect: 0.5

Search: 425026 seqs, 13239027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum match 0%

Maximum match 100%

Listing first 45 summaries

Database: 1: SP:Archaea.\*  
2: SP:Bacteria.\*  
3: SP:Eukarya.\*  
4: SP:Human.\*  
5: SP:Invertebrates.\*  
6: SP:Plant.\*  
7: SP:Protozoa.\*  
8: SP:Unclassified.\*  
9: SP:Virus.\*  
10: SP:Unclassified.\*  
11: SP:Unclassified.\*  
12: SP:Unclassified.\*  
13: SP:Unclassified.\*  
14: SP:Unclassified.\*

Prod. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summary

Result	Score	Query	Length	DB ID	Description
1	1759	99.8	350	4	G93426
2	1377	18.5	320	5	G93426
3	1377	18.5	320	5	G93426
4	1377	18.5	320	5	G93426
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32	1377	18.5	320	5	G93426
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34	1377	18.5	320	5	G93426
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36	1377	18.5	320	5	G93426
37	1377	18.5	320	5	G93426
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41	1377	18.5	320	5	G93426
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43	1377	18.5	320	5	G93426
44	1377	18.5	320	5	G93426
45	1377	18.5	320	5	G93426

# ALIGNMENTS

Result	Score	Query	Length	DB ID	Description
1	1759	99.8	350	4	G93426
2	1377	18.5	320	5	G93426
3	1377	18.5	320	5	G93426
4	1377	18.5	320	5	G93426
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42	1377	18.5	320	5	G93426
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44	1377	18.5	320	5	G93426
45	1377	18.5	320	5	G93426























Db 1777 -----LARIKALNINSLVAMNAPLELIVAYT LAYPISLARSATLITINITS 1778  
 Db 116 L-----FSEFYVLOLARS-----ERYVKAANVEDSVTLA-OLARIPFENS 164  
 Db 1779 LCTGSLJBSSTVOVLRSLTSPISLPTLITSVKASVAVAFSSVRSFSGY 188  
 Oy 165 -LSSP-JNLSNNVOLLFLFELVOYHISL-----LERNIKAL-----DISPOLSELA 217  
 Db 1839 EREYATLELVEYLA-LELME-ACRHOPIELCMQDWTLELOFRVAVTSLDRAVLY 1896  
 Oy 218 GLDICKER-VEBSPDPSDKTLVLAORFADMS-----LERNIKAL-----DISPOLSELA 217  
 Db 1897 VEGTISRVSODIOTLITSLMSLCKL-----GDTNVOYLLEAVYALMPLAND 1934  
 Oy 254 -----LGNAAVVL- VYVSPISLPTLTLETLEKONKAP-----292  
 Db 1955 SPULAKLVANVAVLODENVTLASGTALELONITLTLFTRKSPREYMAIRMPLE 2014  
 Oy 293 -----TALATKIVTSYVNNY 210  
 Db 2015 WHCKOHHVGLJNSNFWALVHLL 2041

RESULT 4  
 PCT-US94-00198-2  
 Sequence 2, Application PCT/US94/00198

GENERAL INFORMATION:  
 TITLE OF INVENTION: PAS Associated GAB Proteins  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Schering Corp.  
 STREET: 1 Guild Farms  
 STATE: Kenilworth  
 COUNTRY: USA  
 ZIP: 94104-1104  
 COMPLETION DATE: 08/07/95  
 COMPUTER: SUN-486i, 3.0  
 SOFTWARE: SYSDRAW, 2.0  
 MEDIUM TYPE: floppy disk  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/00198  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA: US 08/004,924  
 FILING DATE: 08/04/93  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LAM, Paul G.  
 ADDRESS: 32 743  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 822-7095  
 TELEFAX: (201) 822-7095  
 INFORMATION FOR SEQ ID NO: 2:  
 LENGTH: 248  
 TYPE: amino acids  
 STRANDNESS: single  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE: Homo sapiens  
 PCT-US94-00198-2

Query Match 5.7% Score 100.5 Db 55 Length 2685;  
 Best Local Similarity 22.2% Pctd. No. 1:1; Indels 101; Gaps 18;  
 Mismatches 86; Conservative 60; Mismatches 140;

Oy 113 CYLZGHSILASQSVFKNQWTFE-----REYVAKSMKSVKESLSPVLA 65  
 Db 1667 GGLDSKASVADVAVLASVAVKSVKSVKCKLDTGCTSLTQVLMQIMDLAI 1726  
 Oy 66 GALTFRATVQVQVQVCLLAPG-----SVYSLANAPSLIC-----VANHS 115  
 Db 1777 -----LARIKALNINSLVAMNAPLELIVAYT LAYPISLARSATLITINITS 1778  
 Oy 116 L-----FSEFYVLOLARS-----ERYVKAANVEDSVTLA-OLARIPFENS 164  
 Db 1779 LCTGSLJBSSTVOVLRSLTSPISLPTLITSVKASVAVAFSSVRSFSGY 188  
 Oy 165 -LSSP-JNLSNNVOLLFLFELVOYHISL-----LERNIKAL-----DISPOLSELA 217  
 Db 1839 EREYATLELVEYLA-LELME-ACRHOPIELCMQDWTLELOFRVAVTSLDRAVLY 1896  
 Oy 218 GLDICKER-VEBSPDPSDKTLVLAORFADMS-----LERNIKAL-----DISPOLSELA 217  
 Db 1897 VEGTISRVSODIOTLITSLMSLCKL-----GDTNVOYLLEAVYALMPLAND 1934  
 Oy 254 -----LGNAAVVL- VYVSPISLPTLTLETLEKONKAP-----292  
 Db 1955 SPULAKLVANVAVLODENVTLASGTALELONITLTLFTRKSPREYMAIRMPLE 2014  
 Oy 293 -----TALATKIVTSYVNNY 210  
 Db 2015 WHCKOHHVGLJNSNFWALVHLL 2041

RESULT 5  
 US-08-510-284-1  
 Patent No. 5,680,955

GENERAL INFORMATION:  
 APPLICANT: NUTRISCI, M. S. A.; MERCK, HITCHCOCK, INC.  
 TITLE OF INVENTION: TO REVERSE ACTIVATED PAS INDUCED MALIGNANT TRANSFORMATION I  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Felte & Lynch  
 STREET: 405 Third Avenue  
 STATE: New York  
 COUNTRY: USA  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
 COMPUTER: IBM PS/2-DOCS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 FILING DATE: 09/08/90  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/071,575  
 FILING DATE: 1-JUNE-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LAM, Paul G.  
 ADDRESS: 32 743  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 822-7095  
 TELEFAX: (201) 822-7095  
 INFORMATION FOR SEQ ID NO: 1:  
 LENGTH: 2818  
 TYPE: amino acid  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE: Human  
 PUBLICATION INFORMATION:  
 AUTHORS: Merck, Douglas A.; Saulino, Ann M.;



COMPILED: IBM PC COMPATIBLE  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: 09/4/9, 933  
FILE NAME: 25 MAY 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION: P.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 2044-2055.10  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 942-0932  
INFORMATION FOR SEQ ID NO: 2  
SEQUENCE CHARACTERISTICS: 2  
LENGTH: 2818 amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE: UNKNOWN  
POSITION IN GENOME: CHROMOSOME/SEGMENT: 17q11.2  
NAME/TEXT: cleavage-site  
LOCATION: group(583..586, 815..818, 2573..2576, 2810..2813)  
OTHER INFORMATION: /note="Potential cleavage site"  
FEATURE: OTHER INFORMATION: /note="Potential cleavage site"  
NAME/TEXT: modified-site  
OTHER INFORMATION: /note="Potential cleavage site"  
FEATURE: OTHER INFORMATION: /note="Potential cleavage site"  
LOCATION: group(1264..1276, 1358..1377, 1389..1390, 1391, 1392, 1393, 1400, 1423, 1426, 1428, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1560, 1561, 1562, 1563, 1564, 1565, 1566, 1567, 1568, 1569, 1570, 1571, 1572, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 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Mon Aug 20 10:21:55 2001

us-09-284-320-6.ra1

Page 10

Search completed: July 3, 2001, 16:18:53  
Job time: 165 sec



GenCode version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2001, 18:14:09 ; Search time 5416.15 seconds

2987/517 Million cell updates/sec

Title: US-09-284-320-31

Perfect score: 1050

Sequence: 1 atgcgcgtctctctcgtc.....accgaagatccatgcat 1050

Scoring table: IDENTITY MNC

Gapop 10.0 ; Gapext 1.0

Searched: 1144157 seqs, 773387458 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Genbank:
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3: gb_ha3.*
4: gb_ha4.*
5: gb_ha5.*
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43: gb_ha43.*
44: gb_ha44.*
45: gb_ha45.*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Rank	No.	Score	Match	Length	DB ID	Description
1	2	1490.4	94.3	1884	93	US0800272
2	3	860.4	81.9	158239	80	AL156115
3	4	858.8	81.3	158572	80	AL156115
4	5	491	46.8	622	97	HS171795
5	6	153	18.4	129543	68	AC026156
6	7	153	18.3	129543	69	AC026156
7	8	153	18.3	129543	69	AC026156









Db 19666 AACGATGATGACATGCTGCTACACACGAGCATGCTTACACCTTGCGAAGT 19667  
 Oy 301 GAGTCTCTGCTGCTGAGGATGATGATGATGATGATGATGATGATGATGAT 19668  
 Db 19666 CAGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19667  
 Oy 361 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
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 Oy 421 AATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 Db 199486 AATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199427  
 Oy 481 AATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 Db 199426 GAAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199367  
 Oy 541 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 Db 199366 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199307  
 Oy 601 AATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
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 Oy 661 AATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 Db 199246 GAAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199188  
 Oy 721 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
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 Oy 781 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
 Db 199127 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199068  
 Oy 841 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 Db 199067 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9014  
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RESULT 5  
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 VERSION AL36381.7 GI:10038994  
 KEYWORDS HPG, HPG3, PHAGE1, BTOS, DRAPE.  
 SOURCE human.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE PubMed  
 Title Khamisli, I. to 195817)  
 Journal Direct Submission  
 Accession (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 UK  
 Request: Clonerequest@sanger.ac.uk

COMMENT  
 On Sep 9, 2000 this sequence version replaced gi|19797513.  
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 Sanger Centre  
 Genome Center  
 Wellcome Trust  
 Contact: hampster@sanger.ac.uk  
 Contact: hampster@sanger.ac.uk  
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 Project Information  
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 Summary Statistics  
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 Assembly program XG864; version 4.5  
 Chemistry type PCR; primer 150 bp; 1000 cycles  
 Consensus quality: 19568 bases at least Q40  
 Consensus length: 1000 bp  
 Insert size: 164017; 3.2% error; average-  
 Insert size: 174497; 3.2% error; average-  
 Coverage: 21 in Q40 bases; average-  
 Coverage: 21 in Q40 bases; average-  
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 NOTE: This is a working draft sequence. It currently  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 dashes. This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preselected. 8100: contig of 810 bp in length  
 8111 8210: gap of 100 bp  
 8112 8210: contig of 1064 bp in length  
 13655 13954: contig of 300 bp in length  
 13955 46963: contig of 3363 bp in length  
 46964 47093: gap of 100 bp  
 47094 47093: contig of 100 bp in length  
 59515 59643: gap of 100 bp  
 59615 59643: contig of 27203 bp in length  
 86918 90065: contig of 3148 bp in length  
 90066 90165: gap of 100 bp  
 90166 90165: contig of 11693 bp in length  
 101951 101951: contig of 3512 bp in length  
 101951 105700: contig of 3512 bp in length  
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 109112 109211: gap of 100 bp  
 109212 113889: contig of 1378 bp in length  
 113890 113889: contig of 100 bp in length  
 113890 124809: gap of 100 bp  
 124810 124809: gap of 100 bp  
 124810 124809: contig of 3414 bp in length  
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 124842 140194: contig of 1171 bp in length  
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 149123 149222: gap of 100 bp  
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ACCESSION AC026156 12643 bp NM\_284967-200  
VERSION AC026156 12643 bp NM\_284967-200  
KEYWORDS AC026156 12643 bp NM\_284967-200

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 12643) Dong M., Wen M., Xu S., Gu W., Tu Y., Jia J., Ni C., Zhou C., Zhou M., Zhou Y., Ren S., Fu G., Chen Z., and Huang M.

Submitted (21-Apr-2000) Genomic part., Chinese National Human Genome Center at Shanghai, 315 Shou Jing Road, Shanghai, China

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Genome Center, Chinese National Human Genome Center at Shanghai

Genome Center, Chinese National Human Genome Center at Shanghai

DB 8982 TTTTGTCTCTCAAGT 8985

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VERSION AC026156 12643 bp NM\_284967-200  
KEYWORDS AC026156 12643 bp NM\_284967-200

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 12643) Dong M., Wen M., Xu S., Gu W., Tu Y., Jia J., Ni C., Zhou C., Zhou M., Zhou Y., Ren S., Fu G., Chen Z., and Huang M.

Submitted (21-Apr-2000) Genomic part., Chinese National Human Genome Center at Shanghai, 315 Shou Jing Road, Shanghai, China

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Genome Center, Chinese National Human Genome Center at Shanghai

DB 89704 AATATTCAGATCTTCAAGT 89657

RESULT 10

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SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 12643) Dong M., Wen M., Xu S., Gu W., Tu Y., Jia J., Ni C., Zhou C., Zhou M., Zhou Y., Ren S., Fu G., Chen Z., and Huang M.

Submitted (21-Apr-2000) Genomic part., Chinese National Human Genome Center at Shanghai, 315 Shou Jing Road, Shanghai, China

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[illegible][illegible]

Query Match	12.6%	Score 132.2;	DB 94;	Length 72831;
Best Local Similarity	91.5%;	Pred. No. 1.7e-27;		
Matches 140;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0;









Project and the Washington University Genome Sequencing Center.  
For additional information about the map position of this sequence,  
see <http://www.hbmap.nih.gov/DIR/GB/CH7> or send an E-mail to  
greenh@hgti.nih.gov

**SOURCE INFORMATION:**  
This clone is from a release of the human BAC library. The library  
was prepared from a human fibroblast cell line (H1h7) by Dr.  
Shizuya at the Fredrick Prossman Lab, Sci. 99-074-9727 (1992). Kim et  
al., Genomics 34:213-218 (1996).

**VECTOR:** pBESD  
**Selection:** chloramphenicol

**NEIGHBORING SEQUENCE INFORMATION:**  
This clone overlaps position 1 of H1h73609;  
actual and is at 155537 of H1h73609. This clone lies in an  
unanchored cluster of unknown orientation.

This clone contains **SSS3233** (MIM:911312).

**Location/Qualifiers**

1. 155537 Homo sapiens\*

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misc-feature 20135..21945

/note="Probable pseudogene. Similar to NSRPALPHA U28366

(NM009993281)." 20132..48208

misc-feature 20132..48208

/note="Probable pseudogene. Similar to human EST U56844 (MIM:9138715)

2039002..21130 to human EST U56844 (MIM:9138715)

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using SW model

Run on: August 18, 2001, 19:15:13 ; Search time 250.24 Seconds  
(without alignments)

Title: US-09-284-320-31

Sequence: 1 atggtctgtcttgcgtct.....accgaagatctgaatgat 1050

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues  
Total number of hits satisfying chosen parameters:

```
Minimum DB seq length: 0
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Maximum no. seq. aligned: 20000000

Maximum Match 100%

Database :

1. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1360.DAT.\*
2. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1361.DAT.\*
3. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1362.DAT.\*
4. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1363.DAT.\*
5. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1364.DAT.\*
6. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1365.DAT.\*
7. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1366.DAT.\*
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9. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1368.DAT.\*
10. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1369.DAT.\*
11. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1370.DAT.\*
12. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1371.DAT.\*
13. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1372.DAT.\*
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23. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1400.DAT.\*
24. /cgm1\_3/gcgcchla/geneseq/geneseq/NA1401.DAT.\*

## SUMMARIES

	No.	Score	Query Match	Length	ID	Description
	1	1050	100.0	1050	AAV9561	human epidermal co
	2	1050	100.0	1053	AAV9561	human epidermal co
	3	1050	100.0	1058	AAV9574	human epidermal co
	4	1048.4	99.8	1099.22	AAV9774	human CDKN encoding
	5	1048.4	99.8	1099.22	AAV9774	human CDKN encoding
	6	1048.4	99.8	1099.22	AAV9774	human CDKN encoding
	7	380.8	37.2	380.8	AAV9370	human restricted pro
	8	386.2	36.8	850	AAV19733	Ptine-specific fo
	9	386.2	36.8	850	AAV19733	Ptine-specific fo
	10	166.2	15.8	454	AAV1203	human gene express
	11	153.8	14.6	459.21	AAV1203	Xenopus restricte

[illegible]

## RESULT 1

1

ID	AAV49561 standard; cDNA to mRNA; 1050 BP
AY	

AAV4 9561, AC

DT 21-OCT-1998 (first entry)

DE Human epidermal carcinoma cell line KB clone HP01293 cDNA #2

km Transmembrane domain; human; nutrition; cytokine; cell proliferation  
km differentiator; immune system; stimulator; suppressor; regulator

KW haemostatic; thrombolytic; ligand; anti-inflammatory; tumour; ds.  
 KW haematopoiesis; activin; inhibitor; chemotactic; chemokinetic; receptor  
 KW haemostatic; thrombolytic; ligand; anti-inflammatory; tumour; ds.

05 Homo sapiens.

PN W09821328-A2

PD 22-MAY-1998.  
XX

01 OCT - NOV - 10  
XX

XX

PA (SAGA ) SAGAMI CHEM RES CENTRE  
XX

PI Kato S, Kobayashi M, Sekine S, Iimadeguchi T,  
XX

DR P-PSDB; AAM64539.

P7 Human protein having transmembrane domain - useful for, e.g.



























